

## SEQUENCE LISTING

&lt;110&gt; Suntory Limited

&lt;120&gt; MARCHANTIALES-DERIVED UNSATURATED FATTY ACID SYNTHETASE GENES

AND USE OF THE SAME

&lt;130&gt;

&lt;150&gt; JP 2003-425673

&lt;151&gt; 2003-12-22

&lt;160&gt; 46

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 2519

&lt;212&gt; DNA

&lt;213&gt; Marchantia polymorpha

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (253)..(1698)

&lt;400&gt; 1

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gtcggactga tcaactcagtc cgtcactgca aacgcgagcg agcgagagtg cgagtgagcg 180

agcgagcgag cgagagccgc ggtgtgtctg tgagatccaa tccttttct gctttgcgcg 240

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Met Ala Ser Ser Thr Thr Thr Ala Val Lys Gln Ser Ser

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Gly Gly Leu Trp Ser Lys Trp Gly Thr Gly Ser Asn Leu Ser Phe Val

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Ser Arg Lys Glu Gln Gln Gln Gln Gln Gln Ser Ser Pro Glu Ala

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tcg act ccc gcg gcg cag cag gag aaa tcc atc agt aga gaa tcc atc 435

Ser Thr Pro Ala Ala Gln Gln Glu Lys Ser Ile Ser Arg Glu Ser Ile

50 55 60



Asn Val His His Ala Ala Thr Asn Glu Cys Asp Asp Lys Tyr Gln Pro  
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 Ile Asp Pro Asp Ile Asp Thr Val Pro Leu Leu Ala Trp Ser Lys Glu  
 270 275 280 285

atc ttg gcc acc gtc gac gac caa ttc ttc cga tcg atc atc agc gtg 1155  
 Ile Leu Ala Thr Val Asp Asp Gln Phe Phe Arg Ser Ile Ile Ser Val  
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cag cac ctt ctg ttc ttc ccg ctc ctc ttc ttg gca aga ttc agc tgg 1203  
 Gln His Leu Leu Phe Phe Pro Leu Leu Phe Leu Ala Arg Phe Ser Trp  
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ctg cat tcg agt tgg gcc cac gcc agc aac ttc gag atg cct cgg tac 1251  
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gct gcg aaa gta tag atcgacgaga gttcccacc aacacagtta gaacaaggga 1738  
 Ala Ala Lys Val  
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<211> 481

<212> PRT

<213> Marchantia polymorpha

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35 40 45

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 Phe Leu Thr Val Glu Glu Val Ser Lys His Asp Asn Pro Ser Asp Cys  
 65 70 75 80  
 Trp Ile Val Ile Asn Asp Lys Val Tyr Asp Val Ser Ala Phe Gly Lys  
 85 90 95  
 Thr His Pro Gly Gly Pro Val Ile Phe Thr Gln Ala Gly Arg Asp Ala  
 100 105 110  
 Thr Asp Ser Phe Lys Val Phe His Ser Ala Lys Ala Trp Gln Phe Leu  
 115 120 125  
 Gln Asp Leu Tyr Ile Gly Asp Leu Tyr Asn Ala Glu Pro Val Ser Glu  
 130 135 140  
 Leu Val Lys Asp Tyr Arg Asp Leu Arg Thr Ala Phe Met Arg Ser Gln  
 145 150 155 160  
 Leu Phe Lys Ser Ser Lys Met Tyr Tyr Val Thr Lys Cys Val Thr Asn  
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 Phe Ala Ile Leu Ala Ala Ser Leu Ala Val Ile Ala Trp Ser Gln Thr  
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 Tyr Leu Ala Val Leu Cys Ser Ser Phe Leu Leu Ala Leu Phe Trp Gln  
 195 200 205  
 Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val Thr Glu  
 210 215 220  
 Asn Arg Ser Leu Asn Thr Tyr Phe Gly Gly Leu Phe Trp Gly Asn Phe  
 225 230 235 240  
 Ala Gln Gly Tyr Ser Val Gly Trp Trp Lys Thr Lys His Asn Val His  
 245 250 255  
 His Ala Ala Thr Asn Glu Cys Asp Asp Lys Tyr Gln Pro Ile Asp Pro  
 260 265 270  
 Asp Ile Asp Thr Val Pro Leu Leu Ala Trp Ser Lys Glu Ile Leu Ala  
 275 280 285  
 Thr Val Asp Asp Gln Phe Phe Arg Ser Ile Ile Ser Val Gln His Leu  
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 Leu Phe Phe Pro Leu Leu Phe Leu Ala Arg Phe Ser Trp Leu His Ser  
 305 310 315 320  
 Ser Trp Ala His Ala Ser Asn Phe Glu Met Pro Arg Tyr Met Arg Trp  
 325 330 335  
 Ala Glu Lys Ala Ser Leu Leu Gly His Tyr Gly Ala Ser Ile Gly Ala  
 340 345 350  
 Ala Phe Tyr Ile Leu Pro Ile Pro Gln Ala Ile Cys Trp Leu Phe Leu  
 355 360 365  
 Ser Gln Leu Phe Cys Gly Ala Leu Leu Ser Ile Val Phe Val Ile Ser  
 370 375 380  
 His Asn Gly Met Asp Val Tyr Asn Asp Pro Arg Asp Phe Val Thr Ala  
 385 390 395 400  
 Gln Val Thr Ser Thr Arg Asn Ile Glu Gly Asn Phe Phe Asn Asp Trp  
 405 410 415  
 Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro Ser  
 420 425 430  
 Leu Pro Arg His Asn Leu Ala Lys Val Ala Pro His Val Lys Ala Leu  
 435 440 445

Cys Ala Lys His Gly Leu His Tyr Glu Glu Leu Ser Leu Gly Thr Gly  
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 <213> Marchantia polymorpha

<220>  
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 <222> (194)..(1066)

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 cgaatccgcc gagagtcgat cgggattggg tagaaggagg agaaggagga gaagaggagg 180  
 aggaggagca gcg atg gag gcg tac gag atg gtg gat agt ttt gtg tcg 229  
                   Met Glu Ala Tyr Glu Met Val Asp Ser Phe Val Ser  
                   1                      5                      10  
 aag acg gtt ttc gaa acg ctg cag aga ctg agg ggc gga gtc gtg ttg 277  
 Lys Thr Val Phe Glu Thr Leu Gln Arg Leu Arg Gly Gly Val Val Leu  
                   15                      20                      25  
 acg gaa tct gcg atc acc aaa ggt ttg cca tgc gtc gat agc ccg acg 325  
 Thr Glu Ser Ala Ile Thr Lys Gly Leu Pro Cys Val Asp Ser Pro Thr  
                   30                      35                      40  
 ccg atc gtt ctt ggg ttg tgc tcc tac ttg aca ttc gtg ttt ctc ggg 373  
 Pro Ile Val Leu Gly Leu Ser Ser Tyr Leu Thr Phe Val Phe Leu Gly  
                   45                      50                      55                      60  
 ctc att gtc atc aag agc ctg gat ctt aag ccc cgc tcc aag gag ccc 421  
 Leu Ile Val Ile Lys Ser Leu Asp Leu Lys Pro Arg Ser Lys Glu Pro  
                   65                      70                      75  
 gcc att ttg aac ctg ttt gtg atc ttc cac aac ttc gtc tgc ttc gca 469  
 Ala Ile Leu Asn Leu Phe Val Ile Phe His Asn Phe Val Cys Phe Ala  
                   80                      85                      90  
 ctc agt ctg tac atg tgc gtg gga att gtc cgt caa gct atc ctc aac 517  
 Leu Ser Leu Tyr Met Cys Val Gly Ile Val Arg Gln Ala Ile Leu Asn

95	100	105	
agg tac tct ctg tgg ggc aat gcg tac aat ccc aaa gaa gtt caa atg 565			
Arg Tyr Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys Glu Val Gln Met			
110	115	120	
ggc cac ctg ctc tac att ttc tac atg tca aag tac atc gag ttt atg 613			
Gly His Leu Leu Tyr Ile Phe Tyr Met Ser Lys Tyr Ile Glu Phe Met			
125	130	135	140
gac acg gtc att atg att ttg aag cgc aac acg cgc cag atc act gtg 661			
Asp Thr Val Ile Met Ile Leu Lys Arg Asn Thr Arg Gln Ile Thr Val			
145	150	155	
ttg cat gtg tac cac cac gca tcc atc tcc ttc atc tgg tgg atc atc 709			
Leu His Val Tyr His His Ala Ser Ile Ser Phe Ile Trp Trp Ile Ile			
160	165	170	
gcc tac cat gct cct ggc ggt gaa gct tat ttc tct gcc gca ttg aac 757			
Ala Tyr His Ala Pro Gly Gly Glu Ala Tyr Phe Ser Ala Ala Leu Asn			
175	180	185	
tcc gga gta cat gtg ctc atg tac ctc tac tac ctt ttg gca gca act 805			
Ser Gly Val His Val Leu Met Tyr Leu Tyr Tyr Leu Leu Ala Ala Thr			
190	195	200	
ctg gga aag aac gag aaa gct cgc cgc aag tac cta tgg tgg gga aaa 853			
Leu Gly Lys Asn Glu Lys Ala Arg Arg Lys Tyr Leu Trp Trp Gly Lys			
205	210	215	220
tac ttg aca cag ctg cag atg ttc cag ttt gtc ctt aac atg att cag 901			
Tyr Leu Thr Gln Leu Gln Met Phe Gln Phe Val Leu Asn Met Ile Gln			
225	230	235	
gct tac tac gat att aag aac aac tcg cct tac cca caa ttt ttg atc 949			
Ala Tyr Tyr Asp Ile Lys Asn Asn Ser Pro Tyr Pro Gln Phe Leu Ile			
240	245	250	
cag att ttg ttc tac tac atg atc tcg ctt tta gcg cta ttt gga aac 997			
Gln Ile Leu Phe Tyr Tyr Met Ile Ser Leu Leu Ala Leu Phe Gly Asn			
255	260	265	
ttt tac gtt cac aaa tac gta tca gcg ccc gca aaa cct gcg aag atc 1045			
Phe Tyr Val His Lys Tyr Val Ser Ala Pro Ala Lys Pro Ala Lys Ile			
270	275	280	
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Lys Ser Lys Lys Ala Glu			
285	290		

actaaactgt agtttagca cccatcggtg acacgaatac attctgggtc tgcctgtctt 1156  
 ggaagagtcg aagcattcag gagctctccc gttccatcga tcaaactcgg aacgaagtgc 1216  
 accttttagc tgcgatgaga gtctttactt cctgagccgt cgttcttgat gtggtctgta 1276  
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 ggtaacaaa atcacagttt tgggccctta gttagtgaca accaacccta acactttgat 1456  
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 <212> PRT  
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 35 40 45  
 Gly Leu Ser Ser Tyr Leu Thr Phe Val Phe Leu Gly Leu Ile Val Ile  
 50 55 60  
 Lys Ser Leu Asp Leu Lys Pro Arg Ser Lys Glu Pro Ala Ile Leu Asn  
 65 70 75 80  
 Leu Phe Val Ile Phe His Asn Phe Val Cys Phe Ala Leu Ser Leu Tyr  
 85 90 95  
 Met Cys Val Gly Ile Val Arg Gln Ala Ile Leu Asn Arg Tyr Ser Leu  
 100 105 110  
 Trp Gly Asn Ala Tyr Asn Pro Lys Glu Val Gln Met Gly His Leu Leu  
 115 120 125  
 Tyr Ile Phe Tyr Met Ser Lys Tyr Ile Glu Phe Met Asp Thr Val Ile  
 130 135 140  
 Met Ile Leu Lys Arg Asn Thr Arg Gln Ile Thr Val Leu His Val Tyr  
 145 150 155 160  
 His His Ala Ser Ile Ser Phe Ile Trp Trp Ile Ile Ala Tyr His Ala  
 165 170 175  
 Pro Gly Gly Glu Ala Tyr Phe Ser Ala Ala Leu Asn Ser Gly Val His  
 180 185 190  
 Val Leu Met Tyr Leu Tyr Tyr Leu Leu Ala Ala Thr Leu Gly Lys Asn



195	200	205	
Glu Lys Ala Arg Arg Lys Tyr Leu Trp Trp Gly Lys Tyr Leu Thr Gln			
210	215	220	
Leu Gln Met Phe Gln Phe Val Leu Asn Met Ile Gln Ala Tyr Tyr Asp			
225	230	235	240
Ile Lys Asn Asn Ser Pro Tyr Pro Gln Phe Leu Ile Gln Ile Leu Phe			
245	250	255	
Tyr Tyr Met Ile Ser Leu Leu Ala Leu Phe Gly Asn Phe Tyr Val His			
260	265	270	
Lys Tyr Val Ser Ala Pro Ala Lys Pro Ala Lys Ile Lys Ser Lys Lys			
275	280	285	
Ala Glu			
290			

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 <212> DNA  
 <213> Marchantia polymorpha

<220>  
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 <222> (375)..(1829)

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 tcacgtcgc ccgtgggtgc agatcttccg gattctcat gcgcggatcg tggctgctt 360  
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 Met Pro Pro His Ala Pro Asp Ser Thr Gly Leu Gly  
 1 5 10  
 ccc gaa gtt ttc cgc ctg cct gat gac gcg atc ccg gcc cag gat cgc 458  
 Pro Glu Val Phe Arg Leu Pro Asp Ala Ile Pro Ala Gln Asp Arg  
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 aga tct aca cag aag aaa tac tcg ctt tca gac gtc agc aag cac aac 506  
 Arg Ser Thr Gln Lys Lys Tyr Ser Leu Ser Asp Val Ser Lys His Asn  
 30 35 40

act ccg aat gat tgc tgg ctc gta att tgg ggg aag gtg tac gat gtt 554  
 Thr Pro Asn Asp Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val  
 45 50 55 60

act tcg tgg gtt aag gtc cat cca ggt gga agt ctc atc ttt gtg aag 602  
 Thr Ser Trp Val Lys Val His Pro Gly Gly Ser Leu Ile Phe Val Lys  
 65 70 75

gcg gga cag gat tca aca caa ctc ttt gat tct tat cac ccc ctc tat 650  
 Ala Gly Gln Asp Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr  
 80 85 90

gtc aga aag cta ctt gca cag ttc tgc att ggt gaa ctc caa acg agt 698  
 Val Arg Lys Leu Leu Ala Gln Phe Cys Ile Gly Glu Leu Gln Thr Ser  
 95 100 105

gcg gga gat gag aag ttc aag tct tca acg ttg gag tat gct ggt gaa 746  
 Ala Gly Asp Glu Lys Phe Lys Ser Ser Thr Leu Glu Tyr Ala Gly Glu  
 110 115 120

gaa cat gaa gta ttt tac cac act ctc aag cag cgc gtg gaa acg tac 794  
 Glu His Glu Val Phe Tyr His Thr Leu Lys Gln Arg Val Glu Thr Tyr  
 125 130 135 140

ttc cgc aag cag aag ata aat cct cga tac cat ccg caa atg ctt gtg 842  
 Phe Arg Lys Gln Lys Ile Asn Pro Arg Tyr His Pro Gln Met Leu Val  
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aag tca gcc gtg atc att gga acc ctt ctt ctc tgt tac tat ttt ggc 890  
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 160 165 170

ttc ttc tgg tct caa aat gta ctc ctc tcg atg ttt ctg gca agc atc 938  
 Phe Phe Trp Ser Gln Asn Val Leu Leu Ser Met Phe Leu Ala Ser Ile  
 175 180 185

atg ggg ttc tgc act gcg gag gtg ggc atg tcc atc atg cac gat ggt 986  
 Met Gly Phe Cys Thr Ala Glu Val Gly Met Ser Ile Met His Asp Gly  
 190 195 200

aac cac gga tcg tac aca caa tct acc ttg ctt ggt tac gtc atg ggc 1034  
 Asn His Gly Ser Tyr Thr Gln Ser Thr Leu Leu Gly Tyr Val Met Gly  
 205 210 215 220

gcc act ctt gat ctg gtg gga gct agc agt ttc atg tgg agg cag cag 1082  
 Ala Thr Leu Asp Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln  
 225 230 235

cat gtg gcc ggg cac cac tcg ttc acc aac atc gac cat tac gat cca 1130  
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Asp Ile Arg Val Lys Asp Pro Asp Leu Arg Arg Val Thr Ser Gln Gln			
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ccc cga aga tgg ttt cac gag tat cag cat atc tac tta gga gta ctc 1226			
Pro Arg Arg Trp Phe His Glu Tyr Gln His Ile Tyr Leu Gly Val Leu			
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tat ggc gtt ctt gcc tta aaa agt gtg ttg att gat gat ttc agc gcc 1274			
Tyr Gly Val Leu Ala Leu Lys Ser Val Leu Ile Asp Asp Phe Ser Ala			
285	290	295	300
ttc ttc agt ggt gct atc ggc cca gta aag ata gct caa atg aca cca 1322			
Phe Phe Ser Gly Ala Ile Gly Pro Val Lys Ile Ala Gln Met Thr Pro			
305	310	315	
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Leu Glu Met Gly Val Phe Trp Gly Gly Lys Val Val Tyr Ala Leu Tyr			
320	325	330	
atg ttt ttg ctc cct atg atg tat ggt caa tac aac att ctt act ttc 1418			
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335	340	345	
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Ile Gly Leu Tyr Ile Leu Ser Gln Leu Val Ala Gly Trp Thr Leu Ala			
350	355	360	
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Ala Glu Thr Asp Gly Gly Lys Ala Lys Ile Pro Ser Gly Trp Ala Glu			
385	390	395	
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Met Gln Val Arg Thr Thr Thr Asn Phe Ser Ser Arg Ser Met Phe Trp			
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Thr His Ile Ser Gly Gly Leu Asn His His Gln Ile Glu His His Leu Phe			
415	420	425	
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Pro Gly Val Cys His Val His Tyr Pro Ser Ile Gln Pro Ile Val Lys			
430	435	440	

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 445 450 455 460

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 Trp Ala Ala Leu Arg Ala His Phe Gln His Leu Lys Asn Val Gly Leu  
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caa gat gga cta cga ctg gat ggc tga actgtgacag catgctttgg 1849  
 Gln Asp Gly Leu Arg Leu Asp Gly  
 480 485

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<210> 6

<211> 484

<212> PRT

<213> Marchantia polymorpha

<400> 6

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 35 40 45  
 Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp Val  
 50 55 60  
 Lys Val His Pro Gly Gly Ser Leu Ile Phe Val Lys Ala Gly Gln Asp  
 65 70 75 80  
 Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr Val Arg Lys Leu  
 85 90 95  
 Leu Ala Gln Phe Cys Ile Gly Glu Leu Gln Thr Ser Ala Gly Asp Glu  
 100 105 110  
 Lys Phe Lys Ser Ser Thr Leu Glu Tyr Ala Gly Glu Glu His Glu Val

(12)

115            120            125  
 Phe Tyr His Thr Leu Lys Gln Arg Val Glu Thr Tyr Phe Arg Lys Gln  
 130            135            140  
 Lys Ile Asn Pro Arg Tyr His Pro Gln Met Leu Val Lys Ser Ala Val  
 145            150            155            160  
 Ile Ile Gly Thr Leu Leu Leu Cys Tyr Tyr Phe Gly Phe Phe Trp Ser  
 165            170            175  
 Gln Asn Val Leu Leu Ser Met Phe Leu Ala Ser Ile Met Gly Phe Cys  
 180            185            190  
 Thr Ala Glu Val Gly Met Ser Ile Met His Asp Gly Asn His Gly Ser  
 195            200            205  
 Tyr Thr Gln Ser Thr Leu Leu Gly Tyr Val Met Gly Ala Thr Leu Asp  
 210            215            220  
 Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Ala Gly  
 225            230            235            240  
 His His Ser Phe Thr Asn Ile Asp His Tyr Asp Pro Asp Ile Arg Val  
 245            250            255  
 Lys Asp Pro Asp Leu Arg Arg Val Thr Ser Gln Gln Pro Arg Arg Trp  
 260            265            270  
 Phe His Glu Tyr Gln His Ile Tyr Leu Gly Val Leu Tyr Gly Val Leu  
 275            280            285  
 Ala Leu Lys Ser Val Leu Ile Asp Asp Phe Ser Ala Phe Phe Ser Gly  
 290            295            300  
 Ala Ile Gly Pro Val Lys Ile Ala Gln Met Thr Pro Leu Glu Met Gly  
 305            310            315            320  
 Val Phe Trp Gly Gly Lys Val Val Tyr Ala Leu Tyr Met Phe Leu Leu  
 325            330            335  
 Pro Met Met Tyr Gly Gln Tyr Asn Ile Leu Thr Phe Ile Gly Leu Tyr  
 340            345            350  
 Ile Leu Ser Gln Leu Val Ala Gly Trp Thr Leu Ala Leu Phe Phe Gln  
 355            360            365  
 Val Ala His Val Val Asp Asp Ala Val Phe Pro Val Ala Glu Thr Asp  
 370            375            380  
 Gly Gly Lys Ala Lys Ile Pro Ser Gly Trp Ala Glu Met Gln Val Arg  
 385            390            395            400  
 Thr Thr Thr Asn Phe Ser Ser Arg Ser Met Phe Trp Thr His Ile Ser  
 405            410            415  
 Gly Gly Leu Asn His Gln Ile Glu His His Leu Phe Pro Gly Val Cys  
 420            425            430  
 His Val His Tyr Pro Ser Ile Gln Pro Ile Val Lys Ala Thr Cys Asp  
 435            440            445  
 Glu Phe Asn Val Pro Tyr Thr Ser Tyr Pro Thr Phe Trp Ala Ala Leu  
 450            455            460  
 Arg Ala His Phe Gln His Leu Lys Asn Val Gly Leu Gln Asp Gly Leu  
 465            470            475            480  
 Arg Leu Asp Gly

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<210> 26

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<210> 27

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<210> 28

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<400> 36  
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acid sequence

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Trp Trp Lys Xaa Lys His Asn  
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<210> 38

<211> 7

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<213> Unknown Organism

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<223> Description of Unknown Organism:conserved amino  
acid sequence

<400> 38

Trp Phe Thr Gly Gly Leu Asn  
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<210> 39

<211> 7

<212> PRT

<213> Unknown Organism

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<223> Description of Unknown Organism:conserved amino  
acid sequence

<400> 39

Val Glu Phe Met Asp Thr Val  
1 5

<210> 40

<211> 7

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<213> Unknown Organism

<220>

<223> Description of Unknown Organism:conserved amino  
acid sequence

<400> 40

Lys Tyr Leu Phe Trp Gly Arg  
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